

**Amendments to the Claims**

This listing of claims will replace all prior versions, and listings of claims in the application.

**Listing of Claims:**

Claims 1-21. (Cancelled)

22. (Currently amended) An isolated polynucleotide comprising ~~a~~ the sequence of nucleotides 1525-1643 of SEQ ID NO: 113 comprising a functional vascular tissue-specific *E. grandis* cOMT promoter.

23. (Currently amended) The isolated polynucleotide of claim 22, wherein the polynucleotide comprises ~~a~~ the sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 60, nucleotides 1-1643 of SEQ ID NO: 113, nucleotides 1019-1643 of SEQ ID NO: 113, nucleotides 1351-1643 of SEQ ID NO: 113, nucleotides 1338-1643 of SEQ ID NO: 113; nucleotides 1159-1643 of SEQ ID NO: 113; and nucleotides 1110-1643 of SEQ ID NO: 113.

24. (Currently amended) The isolated polynucleotide of claim 22, wherein the polynucleotide comprises ~~a~~ the sequence of SEQ ID NO: 113.

25. (Previously presented) A genetic construct comprising a polynucleotide sequence of any one of claims 22-24.

26. (Previously presented) A genetic construct comprising, in the 5'-3' direction:

- (a) a promoter sequence;
- (b) a DNA sequence of interest; and
- (c) a gene termination sequence,

wherein the promoter sequence comprises a polynucleotide sequence of claim 22 or claim 23; wherein said promoter sequence possesses vascular tissue-specific promoter function of the *E.grandis* cOMT gene.

27. (Previously presented) The genetic construct of claim 26, wherein the DNA sequence of interest is operably linked to the promoter in an antisense orientation.

28. (Previously presented) The genetic construct of claim 26, wherein the DNA sequence of interest is a coding sequence operably linked to the promoter in a sense orientation.

29. (Previously presented) The genetic construct of claim 26, wherein the DNA sequence of interest is a RNAi expression construct.

30. (Previously presented) The genetic construct of claim 26, wherein the DNA sequence of interest comprises a non-coding sequence operably linked to the promoter in a sense orientation.

31. (Previously presented) A genetic construct comprising in the 5'-3' direction:

- (a) a promoter sequence;
- (b) a polynucleotide sequence of any one of claims 22-24; and
- (c) a gene termination sequence,

wherein the promoter sequence in (a) comprises a xylem-specific promoter sequence that is different from the polynucleotide sequence of (b).

32. (Currently amended) A genetic construct comprising in the 5'-3' direction:

- (a) a promoter sequence;
- (b) a polynucleotide sequence comprising the sequence of nucleotides 1525-1643 of SEQ ID NO: 113 inserted in said construct as a direct or inverted repeat; and
- (c) a gene termination sequence,

wherein the promoter sequence in (a) comprises a xylem-specific promoter sequence that is different from the polynucleotide sequence of (b). The genetic construct of claim 31, wherein said polynucleotide sequence of (b) is inserted in said construct as a direct or inverted repeat.

33. (Previously presented) A host cell comprising the genetic construct of claim 25.

34. (Previously presented) The host cell of claim 33, wherein the host cell is a plant cell.

35. (Previously presented) A method for identifying a gene responsible for a desired function or phenotype, comprising:

- (a) transforming a plant cell with the genetic construct of claim 26, wherein said DNA sequence of interest comprises said gene;
- (b) cultivating the plant cell under conditions conducive to regeneration and mature plant growth to provide a transgenic plant in which the gene is expressed; and
- (c) comparing the phenotype of the transgenic plant with the phenotype of a non-transformed plant, wherein said transgenic plant possesses the desired phenotype resulting from a change in lignification as compared to said non-transformed plant.

36. (Previously presented) The method of claim 35, wherein said lignification is reduced in said transgenic plant as compared to said non-transformed plant.

37. (Previously presented) The method of claim 35, wherein said promoter sequence directs transcription of said DNA sequence of interest in xylem or a tissue involved in xylogenesis of said transgenic plant.

38. (Currently amended) An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

a polynucleotide comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, a 300-mer, 400-mer, 500-mer or 600-mer of complementary to SEQ ID NO: 12, SEQ ID NO: 60, or nucleotides 1-1643 of SEQ ID NO: 113.

39. (Previously presented) An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

a polynucleotide comprising a 180-mer, a 220-mer, a 250-mer, a 300-mer, 400-mer, 500-mer or 600-mer of SEQ ID NO: 113.

40. (New) A genetic construct comprising in the 5'-3' direction:

- (a) a promoter sequence;
- (b) a polynucleotide sequence of claim 38; and
- (c) a gene termination sequence.